FastDB - Fast Pairwise Comparison of Sequences Release 5.4

Results file seq72-t48453.res made by bobryen on Tue 17 Dec 102 12:58:03-PST.

Query sequence being compared:SEQ72-T48453 (1-151) Number of sequences searched: Number of scores above cutoff: 5 Results of the initial comparison of SEQ72-T48453 (1-151) with: File : seq72compares.pep

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PARAMETERS

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K-tuple		Joining penalty	Window size				
PAM-150	m. 168			0.05	Н	0	
Similarity matrix PA	Threshold level of si	Mismatch penalty	Gap penalty	Gap size penalty	Cutoff score	Randomization group	

SEARCH STATISTICS

Standard Deviation 43.25	Total Elapsed 00:00:00.00
Median 42	
Mean 87	CPU 00:00:00.00
Scores:	Times:

Number of residues: Number of sequences searched: Number of scores above cutoff:

3817 5 5 The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Init. Length Score	Init. Opt. Score Scor	Opt. Score	Sig. Frame	rame
1. q9sr66 2. t48453	T22K18.18 protein. TOIG of: t48453 check: 2431	1309	125	137	0.88	00
1. SEQ72-T48453 (1-151) q9sr66 T22K18	(1-151) T22K18.18 protein.					
Initial Score Residue Identity Gaps	= 125 Optimized Score = 528 Matches = 0 Conservative Substitu	137 SI 80 Mi ptions	Significance Mismatches	cance -	0.88 68 3	
V	WDXXRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	XRXXXXXX	/ (ixxxxi	40 XXXXIXXRGMRXXI	50 KLAXRIXX	×
KSKESAKSTOKKS 780	KSKESAKSTOKK§VDWDSLRKEAEŞĞGRKRERTERTMDYVDWDALRCTDVHKIANIİIKRANINM 780 x 800 810 820	LRCTDVH	TANII:	CKRGMNM 840	MLAERIKA O	\$
60 FLXXXVXXHGXIDI	70 80 90 100 110 LEWLRXXPRDXAKXYLLSIXGLGLKSVECVRLLXLHXAFPVDTNVGRJ	100 LLXLHXX	110 VFPVDTNVGF	-	AVRMGWVPLQ	q -
FINRLVKKHGSID 850	LEWLRDVPPDKAKEYLLSUNGLGI 870	-13	HQIAFPVDINVGE 900		IAVRLGWVPLQ 10	- Q:
130 PLPXXLQLHLLEX	130 140 150 PLPXXLQLHLLEXYPXXXXXQKXLWPR				1	
PLPDELQMHLLEL 920 930	PLPDELOMILLIELYELHYHMITFGKVFCTKVKPNCNACPMKAECRHY 0 930 x 950 x 950	RHY				

2. SEQ72-748453 (1-151) t48453 TOIG of: t48453 check: 2431 from: 1 to: 555 Initial Score = 124 Optimized Score = 134 Significance = 0.86
Residue Identity = 61% Matches = 84 Mismatches = 53
Gaps = 0 Conservative Substitutions = 0

```
Results file seq72-q941x6.res made by bobryen on Tue 17 Dec 102 12:58:40-PST.
                                                                                                                                                                                                                                                                                                                                                                                                         Results of the initial comparison of SEQ72-Q941X6 (1-132) with: File : seq72compares.pep
                                                                                                                                                                                                                                                                                    Query sequence being compared:SEQ72-Q941X6 (1-132)
Number of sequences searched:
Number of scores above cutoff:
5
                                                                                                                  FastDB - Fast Pairwise Comparison of Sequences Release 5.4
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K-tuple

PAM-150 .

Joining penalty Window size 5.00 0.05 Similarity matrix PA.
Threshold level of sim.
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group

20

SEARCH STATISTICS

Standard Deviation 36.96 Total Elapsed 00:00:01.00 Median 30 CPU 00:00:00.90 Mean 69 Scores: Times:

3817 5 5 Number of residues: Number of sequences searched: Number of scores above cutoff: The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

ence Name Description Length Score Sig. Fra
1. q9sr66 T22K18.18 protein. 2. t48453 TOIG of: t48453 check: 2431 555 96 119 0.73 0 3. q941x6 putative FPPsynthasel (Fragme 119 93 115 0.65 0
1. SEQ72-0941X6 (1-132) q9sr66 T22X18.18 protein.
Initial Score = 100 Optimized Score = 121 Significance = 0.84 Residue Identity = 56% Matches
WAXXKAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
60 110 120 LXXXVXXHGXIDLEWIRXXPPDXAKXYLLSTXGLGLKSVECVRLLXLHXXAFPVDTN-GRIAVRLGWPLQP I
LPXXXOXHX
2. SEQ72-0941X6 (1-132) t48453 TOIG_Of:F48453 check: 2431 from: 1 to: 555
Initial Score = 96 Optimized Score = 119 Significance = 0.73 Residue Identity = 54% Matches = 73 Mismatches = 58 Gaps = 1 Conservative Substitutions
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
60 70 80 100 110 120 LXXXVXXHGXIDLEWLRXXPPDXAKX/LLSIXGLGLKSVECVRLLXLHXXAFPVDIN-GRIAVRLGWVPLQP
130 x LPXXXQXHX LPESLQLHILEL 550 x
 SEQ72±Q941X6 (1-132) q941X6) Putative FPPsynthasel (Fragment).
Initial Score = 93 Optimized Score = 115 Significance = 0.65 Residue Identity = 60% Matches = 72 Mismatches = 46 Gaps = 1 Conservative Substitutions = 0
WXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

> 0 < 0 | 0 IntelliGenetics > 0 < > 0 <

FastDB - Fast Pairwise Comparison of Sequences Release 5.4 Results file seq72-049498.res made by bobryen on Tue 17 Dec 102 12:59:47-PST.

Ouery sequence being compared:SEQ72-049498 (1-217) Number of sequences searched: 5 Number of scores above cutoff: 5 Results of the initial comparison of SEQ72-049498 (1-217) with: File : seq72compares.pep

PARAMETERS

Similarity matrix PAM-150 K-tuple 1
Threshold level of sim. 16% Joining penalty 20
Gap penalty 5.00 Window size 217
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Number of residues:

Number of sequences searched:

Number of scores above cutoff:

5

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description		Opt.	Sig. Fr	rame
1. q9srl 2. t484 3. q941: 4. t054	**** 1 standard deviation ab T22X18.18 protein. **** 0 standard deviation fr TOIG of: t48453 check: 2431 Putative FPPsynthasel (Fragme TOIG of: t05430 check: 9156	above mean *** 1309 124 from mean *** 555 95 e 119 84	**** 124 161 **** 95 104 84 94 79 138	1.69 0.16 -0.42 -0.69	0 000
. 049498 EQ72-049498 9sr66	Hypothetical 106.3 KDa protel (1-217) T22K18.18 protein.			0.00	0
Initial Score Residue Identity Gaps	zed Score	161 Signi tutions Misman XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	Significence Mismatches 40	1.69 86 5 5 5 1.4XRIXXX	
SKESAKSTOKKSVI 780 79	SKESAKSTQKKSVDWDŠLRKEAESGGRKRERTERTWDTVDWDALRCTDYHKIANIIKRGMNNWLAERI 780 790 810 820 840 60 70 80 90 110 120	CTDVHKIANI 830		MERI	
XXXXXXXXXELXX.	XXXXXXXXXXELXXXVXXXGIDEWLRXXDSXXXXXXXLLSXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIA	ILKSXECVRLL IKSVECVRLL 890	KLXXXAFPVI 	DINVGRIA DINVGRIA 910	
130	YSO 160 FXYPXXXXXXXXXXIWPRICKLXO	170 190 7 XTLYELHYQMITFGKXFCTKXXPNCNACPM 	3KXFCTKXXI SKXFCTKXXI SKVFCTKVKI	190 FCTKXXPNCNACPM [
200 210 X KXECKYFASAXVSSKXLLEXX : : : : KAECRHYSSARASARLALPEP 960 970 980	200 210 x KXECKYFASAXVSSKXLLEXX N. ::: :: N. ::: :: KAECRHYSSARASARLALPEPEESDRTSVMIHERRSKRKPV 970 980 1000				
2. SEQ72-049498 (1. t48453	(1-217) FOIG of: t48453 check: 2431 from:	ë E	555		
Initial Score Residue Identity Gaps	95 Optimized Score 1 418 Matches	04 Signi 90 Misma ons	ficance -	0 16 74	
	X 10 20 WXXXRXXXXEXXXXXDXXXXXX	RXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	40 EXXRGXXXX	LAXRIXXX	
MKGTLADGKKPTS 400	MKGTLADGKKPTSOWDSLRKDVEGNEGROERNKNNMDSIDYEAII 0 440	AIRRASISEISEAIKERGMNNMKÄVRI 450	IKERGMNM 460	favri	
xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx	0 100 110 120 XFIXXXVXXXGXIDLEWLRXDSXXXXXXLSXXSGCIRSXECVRLLXXXXXAFPVDTNVGRIA	100 SLKSXECVRLL 111 11111 KLKSVECVRLL 510	XLXXXAFPV XLXXXAFPV 	120 DTNVGRIA DTNVGRIA	
130 140 X VRIGLVPLDELPXXVQMHQLFX	130 140 x 150 160 VRIGIUPPLERLPXXVQMHQLFXYPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	-			

3. SEQ72-049498 (1-217) q941x6 Putative FPPsynthasel (Fragment).

550

540

seq72-t05430.res

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Results of the initial comparison of SEQ72-T05430 (1-217) with: File : seq72compares.pep

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																					1110
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																*			*		83-0
																					-1-69
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ares.per																					41 2
rile : sed/zcompares.pep																					-3 88-
ire :																				1 1 1 1 1 1 1	- 4 -
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PARAMETERS Similarity matrix PAM-150 K-tuple Threshold level of sim. 16% 1 Joining penalty Mismatch penalty 5.00 Window size Gap penalty 0.05 Cutoff score 1 Randomization group 0

SEARCH STATISTICS

Standard Deviation 18.94	apsed .00
Standard 18.94	Total Elapsed 00:00:00
Median 80	
Mean 92	CPU 00:00:00.01
Scores:	Times:

Number of residues: 3817
Number of sequences searched: 5
Number of scores above cutoff: 5

The scores below are sorted by initial score. Significance is calculated based on initial score. A 100% identical sequence to the query sequence was not found.

The list of best scores is:

In Length Sc
above 1 from
t48453 check: 2431 555 9 FPPsynthasel (Fragme 119 8 t05430 check: 9156 917 7
1. SEQ72-T05430 (1-217) q9sr66 T22K18.18 protein.
Initial Score = 124 Optimized Score = 161 Significance = 1.69 Residue (dentity = 42% Matches = 93 Mismatches = 86 Gaps
SKESAKSTOKKSYDWDSLRKEAESGGRKRERTERTMDTVDWDALRCTDVHKIANITIKRGMNNMLAERI 7 1 1 1 1 1 1 1 1 1
XXXXXXXXXXXXXXXDLEWLRXXDSXXXXXXLLSXXQLKSXCVRLLXLXXXARPVDTNVQRIA XXXXXXXXXXXXXXXXXILLSXXXXXXXLLSXXQLKSXCVRLLXLXXXARPVDTNVQRIA
130 140 150 160 170 180 190 VRLGLVPLEPLPXXVQNHQLEXYPXXXXQKXLWPRLCKLXQXTLYELHYQMITFGKXFCTKXXFNCNACPM
A00 210 X KXBCKYFASAXVSSKXLUEXX
2. SEQ72-T05430 (1-217) t48453 TOIG Of: t48453 Check: 2431 from: 1 to: 555
Initial Score = 95 Optimized Score = 104 Significance = 0.16 Residue Identity = 41% Matches = 60 Mismatches = 74 Gaps = 10 Conservative Substitutions = 2
WXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
LKKOVEGNIGKQERNKNNNDSIDYEAIRKASISELSEAIREKGMNNNLA 420 430 440 450 460 450 460
140 x/150 160 510 520 530 520 530 520 530 520 530 520 530 520 530 530 530 530 530 530 530 530 530 53

3. SEQ72-T05430 (1-217) q941x6 Putative FPPsynthasel (Fragment).

ores is:

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Results file seq71-t05430.res made by bobryen on Tue 17 Dec 102 13:25:29-PST.
                                                                                                                                                                                                                                                                                                                                                                                                               1 64
                                                                                                                                                 Results of the initial comparison of SEQ71-T05430 (1-88) with: File : seq71compares.pep
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                                                                                                                                                                                                                                                                                                                                                                                                               43-
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Window size
                                                                                                         Query sequence being compared: SEQ71-T05430 (1-88)

Number of sequences searched:

A

Number of scores above cutoff:
                                         FastDB - Fast Pairwise Comparison of Sequences Release 5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-tuple
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Threshold level of sim.
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
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STDEV -9
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 Scores:
 Mean 58 50.08
 Standard Deviation 6.08

 Times:
 CPU 00:00:00.00
 Total Elapsed 00:00:00.00

 Number of residues:
 4350
 4350

 Number of sequences searched:
 4

 Number of scores above cutoff:
 4

SEARCH STATISTICS

Number of scores above cutoff:

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

e :					
Init. Opt. Length Score Score Sig. Frame	0 66.0			₩ — ₩	
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Sco			gni sma	KWX ; ;	rsx
th	917	Ţ	86 Significance = 69 Mismatches = 10ns	TXAKV : TEAKV 450	REG 20
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_ ;	TOIG of: t05430 check: 9156	30	64 Optimized Score = 86 708. Matches = 69 10 Conservative Substitutions	PET - PET	70 FLTON
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ž	1. t05430	1-T(Sco	NKK	50 2GNR 1111
ence	· .	EQ7	ial due	LKI! 400	HXI.
Sequence Name	П	1. SEQ71-T05430 (1-88) t05430 ; TOIG of: t05430 check: 9156 from: 1 to: 917	Initial Score Residue Identity Gaps		47
ี้ ดัง		н	H & 0		

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Results file seq72-q9sr66.res made by bobryen on Tue 17 Dec 102 12:57:35-PST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137
                                                                                                                                                                                                                                                                                                     Results of the initial comparison of SEQ72-Q9SR66 (1-208) with: File : seq72compares.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
                                                                                                                                                                                                                Query sequence being compared:SEQ72-Q9SR66 (1-208)
Number of sequences searched:
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Number of scores above cutoff:
5
                                                                                     FastDB - Fast Pairwise Comparison of Sequences Release 5.4
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PARAMETERS

Similarity matrix	PAM-150	K-tuple		1
Threshold level of sim.	ո. 16%			
Mismatch penalty	-	Joining pena	lty	20
Gap penalty	2.00	Window size	•	208
Gap size penalty	0.05			
Cutoff score	1			
Randomization group	0			
	SEARCH	SEARCH STATISTICS		
Scores:	Mean	Median	Standard Deviation	riation

35.00	Total Elapsed 00:00:00	
58	,	3817 5 5
92	CPU 00:00:01	Number of residues: Number of sequences searched: Number of scores above cutoff:
		Number of residues: Number of sequences Number of scores abo
		of of
	Times:	Number Number Number

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

Δ	**** 1 standard deviation above mean **** 9sr66	1. SEQ72-09SR66 (1-208) q9sr66 \ T22K18.18 protein.	Score = 137 Optimized Score = 176 Significance = 1.29 Identity = 59% Matches = 124 Mismatches = 61 23 Conservative Substitutions = 0	X 10 20 30 40 50 WXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	60 70 80 90 100 110 120 FLXXXVXXHGXIDLEWLKXXPPDXAKXYLLSIXGLGLKSVECVRLLXLHXXAFPVDTNVGRIAVRLGWVPLQ ::: :: : :: : : : :	130 140 150 160 170 180 190 PLPXXLQMHLLXXYPXXXXXQKLLWPRLCKLXQXTLYELHYMITFGKXFCTKXXPNCNACPMKXECRHYSS	200 X AXASARXALPXP \$ \$ 111 ARASARLALPEPEESDRTSVMIHERRSKRKPV
Sequence Name	1. q9sr66	1. SEQ72-09SR66 q9sr66	Initial Score Residue Identity Gaps	KSKESAKSTOK 780	60 FLXXXVXXHGX ::: :: : FLNRLVKKHGS 850	130 PLPXXLQMHLLXX :: PLPDELQMHLL 920 930	200 X AXASARXALPXP % % % ARASARLALPEP

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FastDB - Fast Pairwise Comparison of Sequences Release 5.4 Results file seq71-q95r66.res made by bobryen on Tue 17 Dec 102 11:48:05-PST.

Query sequence being compared: SEQ71-Q95R66 (1-90)
Number of sequences searched:
4
Number of scores above cutoff:

Results of the initial comparison of SEQ71-Q95R66 (1-90) with: File : seq71compares.pep

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PARAMETERS

н		20	06			
K-tuple		Joining penalty	Window size			•
PAM-150	. 16%	1	5.00	0.05	ч	0
Similarity matrix	Threshold level of sim	Mismatch penalty	Gap penalty	Gap size penalty	Cutoff score	Randomization group

SEARCH STATISTICS

Standard Deviation 7.55	Total Elapsed 00:00:00.00	
Median 54		4350 4 4
Mean 59	CPU 00:00:00	Number of residues: Number of sequences searched: Number of scores above cutoff:
	,	of residues: of sequences of scores ab
Scores:	Times:	Number of Number

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

e Sig. Frame	0 1.06 0		1.06	40 FXGRXNSFIAR : : FHGRANSFIAR 540	SSVTO
Init. Opt. Length Score Score	re mean **** 1309 67 80		80 Significance = 69 Mismatches = cons	20 30 XDEEKXKWWXXERXXEY : : : :	OVERWINGSCHEEWG
	**** 1 standard deviation above mean **** T22K18.18 protein.	rotein.	Optimized Score = 80 Matches = 69 Conservative Substitutions	10 PPTXXXXXILMDX ;;; ; ; PPTSRVWKLLMSSIDCDGVDG 510	50 60 70 80 90 MRXVQGNRXFXPWKGSVVDSVVGVFLTQNV-DXSSSAYMXLASXFP 11:
Description	**** 1 T22K18.1	(1-90) T22K18.18 protein.	- 67 - 698 - 9	X KVXLI ; VXYSKKQKPKVQLI 490 500	60 CPWKGSVVDSVVG' [111111111111111111111111111111111111
Sequence Name	1. q9sr66	1. SEQ71-Q95R66 (1-90) .g9sr66) T22K18	Initial Score Residue Identity Gaps	YKKSYEEQKAI 480	50 MXXVQGNXXFX : : MXVVQGNRTFS 550

```
> 0 <
O| |O IntelliGenetics
> 0 <
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4
```

Results file seq71-049498.res made by bobryen on Tue 17 Dec 102 12:55:59-PST.

Query sequence being compared: SEQ71-049498 (1-90) Number of sequences searched: 4 Number of scores above cutoff: 4 Results of the initial comparison of SEQ71-049498 (1-90) with: File : seq71compares.pep

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1	20 90	
K-tuple	Joining penalty Window size	
PAM-150	5.00	•
Similarity matrix	Mismatch penalty Gap penalty Gap size penalty Cutoff score Randomization drown	drost constant

PARAMETERS

SEARCH STATISTICS

Scores:	Mean 60	Median 56	Standard Deviation 6.65
Times:	CPU 00:00:00		Total Elapsed 00:00:00.00
Number of residues:		4350	

Number of sequences searched: 4 Number of scores above cutoff: 4 The scores below are sorted by initial score. Significance is calculated based on initial score. A 100% identical sequence to the query sequence was not found.

Init. Opt. Sequence Name Description Length Score Score S19. Frame
30 TOIG of: t05430 check: 9156 917 66 80 0.90 98 Hypothetical 106.3 kDa protei 917 66 80 0.90
1. SE071-049498 (1-90) t05430 TOIG of: t05430 check: 9156 from: 1 to: 917
Initial Score = 66 Optimized Score = 80 Significance = 0.90 Residue Identity = 70% Matches = 69 Mismatches = 21 Gaps
X 10 20 30 40 KVXLDPETXXWXVLMXXDDKXTXAKWXXEXXFXTRXDLFINRM
50 60 70 80 90 HXLQGNRXEXQWRGSVVDSVVGVFLTON-TDXLSSNAFMXVAAXFP
2. $SEQ71^2O49498$ (1-90) 049498) .Hypothetical 106.3 kDa protein.
Initial Score = 66 Optimized Score = 80 Significance = 0.90 Residue Identity = 70% Matches = 69 Mismatches = 21 Gaps = 8 Conservative Substitutions = 0
X 20 30 40 KYXLDPETXXXWXVLMXDDKXTXAKWXXEXXFYTXDEINRM \$\frac{1}{1}
HXLQGNRXFXQWKGSVVDSVVGVFLTQN-TDXLSSNAFMXVAAXFP
480 490 300 210 V 320

SEARCH STATISTICS

20

Joining penalty Window size

5.00

Similarity matrix PAI
Threshold level of sim.
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group

K-tuple

PAM-150 . 16%

PARAMETERS

 Scores:
 Mean
 Median
 Standard Deviation

 59
 55
 6.65

 Times:
 CPU
 Total Elapsed

 00:00:00:00
 00:00:00:00

Number of residues: 4350 Number of sequences searched: 4 Number of scores above cutoff: 4

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

Sig. Frame	. 0			α – α	
Ē.	1.05		1.05 21 0	FIAF	
Sig	7.		,	A C A C A C A C A C A C A C A C A C A C	ÕIS
re.	80		Significance = Mismatches	20 30 40DXXDEXKXKWWXXERXXFXGRXDSFIAR	SMP
Opt Sco	*		canc	ERXXE	AGTS
Init. Opt. Score Scor	**		ifi	30 WXXEI	NFD
Init. Opt. Length Score Score	ean 7		Sign Mism	KXKV H:11	VPSS
ingt	те тей 1207			20 XDEXK) : : ; SDEQK! 530	VPF
7	abor		e utic	-DXO	SOFE
	lon		= = 3tit	IINSEG 520	AXLA : 4SLA
	**** 1 standard deviation above mean **** t2g36490 protein.		Optimized Score = 80 Matches = 69 Conservative Substitutions	X	80 SSAF! SSAF! 590
	dev		Sco		KLSS
	**** 1 standard At2g36490 protein.		Optimized Score Matches Conservative Sub	10 VXLDDETXXXWXLLL \$;;; ; VDLDDETDRVWKLLL	7 - D N N
	tand	(1-90) A t2g36490 protein.	timi tche nser	DETX OETX DETC	0 LTON LTON 580
ion	1 90	pro		<u> </u>	70 GVFL
Description	** 9364	490	698 99	X KV L I	DSW
esc	** At2	90)		CPRP	60 GSW 1111 GSW 57
		At2		PVK	PWKC
မ		901;	itit	7₽\ [‡] ±1 490	50 80 80 HAVQGDRXFXPWKGSVVDSVVGVFLTQNV-DXLSSSAFMXLASXFP : - : : : : : : : : : : :
Nan	sjąt	360 <u>-</u> 9	Scor	GAI	50 QGDI 0GDI 0GDI
ence	1. q9sjq6	SEQ71,09,	ial due	X 10 20 30 40	50 X MHXVQCDRXFXPWKGSVVDSVVGVFLTQNV-DXLSSSAFWXLASXFP 5
Sequence Name	1	1. SEQ717Q9SJQ6 (1-90) q9sjq6 .) At2g36	Initial Score Residue Identity Gaps	480	
(1)		-	- H O		